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Oy	311	KNADNPSMTYKVEVTCPEKITAKTGCSR	337
		: : : : : : : : : : : : : : :	
Db	192	QNADNPSINFQVTCPEGLTAKTNCKR	218

RESULT 2

ID	Q9JH91	PRELIMINARY;	PRT;	219	AA.
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DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OC
 NCBI_TaxID=42452;
 RN
 RP
 RP SEQUENCE FROM N.A.
 RA Ohnoko K., Ohnuma M., Moriya S., Kudo T.;
 RT "Diverse genes of Family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite *Reticulitermes speratus*,"
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBD databases.
 RL EMBL: AB045172; BAA98042.1; --
 DR HSSP: P43316; 2ENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSTL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 2312 MW; A712EF3FCAB041C CRC64;

Query Match	42.1%	Score	772.5	DB	14	Length	219
Best Local Similarity	66.7%	Pred. NO.	4e-45				
Matches 18; Conservative	26	Mismatches	38	Indels	5	Gaps	3

QY	132	NGVITRRWDDCCCKASCMPGKANYSPVKSQNDGVAL--SDSNAGSGGNGNSYMCNDNQ	190
Db	16	SGRTTRRWDDCCCKASCMEKFAAVALQPDVTCADKGTTRVASNDTVSSCCDGBGGTCYDQA	75
QY	191	PMAVNDILAVGFAFAAASGCGESRWCCSCPELFTFTSYAGKKMYYQVNTNGDLDGSGSTG	250
Db	76	PMAVNDVASVAGFAFAAACCC--GGESGACNCCCELFTFTISGPNAGKKMYYQVNTNGDLDGSGN--	135
QY	251	AHPDLQMPGGGVGIFNGCSSQMGAPNDGWSRYGIISSADCSSLPALQAGCKRPNWF	310
Db	133	-QFDLAIPIGGGVGIVNGCTQQSGAPSPGHWGWSRYGIVSSRECSQPLPSGLQAGCQWTFPMWF	191
QY	311	KNAADNPSMTYKEVYTCPELITAKTGCSR	337
Db	192	QNAADNPSINFPQVTCPELITAKTNCKR	218

RESULT 3

ID Q9JH84 PRELIMINARY; PRT; 220 AA.

DT 01-OCT-2000 (T:EMBLrel. 15, Created)
 DT 01-OCT-2000 (T:EMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (T:EMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onoko K., Ohkuna M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotid
 RT protists in the hindgut of termite *Reticulitermes speratus*.";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB045119; BAA98049.1; -;
 DR HSSP; P43J16; ZENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_Hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CRC64 ;

Query Match	42.1%	Score 772.5	DB 14	Length 220
Best Local Similarity	66.2%	Pred. No. 4e-45	38	Indels 5
Matches 137	Conservative 27	Mismatches		Gaps 3

[illegible]

RESULT 4

ID Q9JH87 PRELIMINARY; PRT; 219 AA.

NC Q52641.1 2000 (TEMBL:rel. 15, Created)
 DT 01-OCT-2000 (ITEMBL:rel. 15, Last sequence update)
 DT 01-OCT-2000 (ITEMBL:rel. 15, Last sequence update)
 DT 01-Mar-2002 (TEMBL:rel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohnoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite *Reticulitermes speratus*,"
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045176; BAA98046.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS0140; GLYCOSYL_HYDROL_P45; UNKNOWN_1
 SQ SEQUENCE 219 AA; 23134 MW; 4BDEFBC9ACC772D CRC64;

Query Match	41.9%	Score 769.5;	DB 14;	Length 219;
Best Local Similarity	63.1%;	Pred. No. 6.4e-45;		
Matches 135; Conservative	32;	Mismatches 42;	Indels 5;	Gaps 3

```

QY      123  VSGGASGNGVTTTTRYNMCCCKASCSPGKKNVSSPVKSCNKKDQVTL-SDSNAGSCCNNGNS 183
Db      9    ISWLSADSGKRTTYMCCCKGSCGMEKKANVDPIPTCKADGTRVASNQTYKSCGCDGGDG 68
QY      184  YMCNDNOPAVYNENLAVGFAAAAISSGGGSEFWCCSCFELTFETSTSVAGKXWVQVINTGG 243
Db      69  FMCIDQIPMVQVSSLSYGFAAAAAC-GESSGACCCGYELFTTSRGVNGKXWVQINTGG 127
QY      244  DLGSGTAHFPIQMFGGVGVIENGCSQMGAINDWGSRVGGISASDPCSSLPALQAGC 303
Db      128  DLGSG--GPDLAIPGGVGVIYNGCTAAGASPDGMSRYGVSSRSECSPQLPGLQAGC 184
QY      304  KKRPNWFKANDNPSSMYKEYTCPKETLATGTGSPR 337
Db      185  QMRFDWFFQANDNPSSINFQSCSEELIATHTQNR 218

```

RESULT 5

Q9JH83 PRELIMINARY; PRT; 220 AA.

AC	Q9JH83;
DT	01-OCT-2000 (Tremblrel. 15, Created)

RT protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045173; BAA98043.1; --

DR HSSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 219 AA; 23037 MW; 372E016415530A9A CRC64;

Query Match 41.5%; Score 762.5; DB 14; Length 219;

Best Local Similarity 64.3%; Pred. No. 1.9e-44;

Matches 134; Conservative 26; Mismatches 41; Indels 5; Gaps 3;

QY 132 NGVTRRYWDCCKAAGSCWPGKAVSSPVKSCNKGDTAL-SDSNAQSGCNGNSYMCNDNP 190

DB 16 SGKTRRYWDCCKAGCGWEKKNVDPIDTCAKDGTTTVAASNDTVKSGCDGDTGMCYDQT 75

QY 191 PMAVNDNLAYGFAPAAAIISGGESRWCCSCFELFTSTSVAGKKVAVVNTGDLGSSGTG 250

DB 76 PMQVSDSLSYGFAPAAACC-GGESGACCGCYELFTTSGPVNGKKMIVQITNTGDLGSSN-- 132

QY 251 AHFLQMPGGGVIIFNGCCSQMGAPNDGWSRGYGISASDSSLPSALQAGCKKRFNFW 310

DB 133 -QFDLAIPIGGGVIINGCTAOSGAPSDGWSRGYGSRSBSCQLPSGLQAGCQMRDWF 191

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 QNADNPISFNVCPSSEIIAKTNCNR 218

RESULT 9

Q9JH93 PRELIMINARY; PRT; 220 AA.

AC Q9JH93; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_Taxid=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045170; BAA98040.1; --

DR HSSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 220 AA; 23091 MW; 35F174F9B79C2D65 CRC64;

Query Match 41.5%; Score 761.5; DB 14; Length 220;

Best Local Similarity 65.0%; Pred. No. 2.2e-44;

Matches 134; Conservative 26; Mismatches 41; Indels 5; Gaps 3;

QY 133 GVTTRRYWDCCKAAGSCWPGKAVSSPVKSCNKGDTAL-SDSNAQSGCNGNSYMCNDNP 191

DB 18 GRTTRRYWDCCKAGCGWEKKNVDPIDTCAKDGTTTVAASNDTVKSGCDGDTGMCYDQT 77

QY 192 MAVNDNLAYGFAPAAAIISGGESRWCCSCFELFTSTSVAGKKVAVVNTGDLGSSGTG 251

DB 78 WGVNDSFALGFAPAAAVS-GGESAACNCNCELTFTSGVNGKKMIVQITNTGDLGSSN-- 133

QY 252 HFDLQMPGGGVIIFNGCCSQMGAPNDGWSRGYGISASDSSLPSALQAGCKKRFNFW 311

DB 134 QFDLAIPIGGGVIINGCTAOSGAPSDGWSRGYGSRSBSCQLPSGLQAGCQMRDWF 193

QY 312 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 194 NADNPISFNVCPSSEIIAKTNCNR 218

RESULT 10

Q9JH88 PRELIMINARY; PRT; 219 AA.

AC Q9JH88; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_Taxid=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045175; BAA98045.1; --

DR HSSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 219 AA; 23030 MW; 175BF1344C6D7024 CRC64;

Query Match 41.4%; Score 760.5; DB 14; Length 219;

Best Local Similarity 64.7%; Pred. No. 2.6e-44;

Matches 134; Conservative 25; Mismatches 43; Indels 5; Gaps 3;

QY 132 NGVTRRYWDCCKAAGSCWPGKAVSSPVKSCNKGDTAL-SDSNAQSGCNGNSYMCNDNP 190

DB 16 SGKTRRYWDCCKAGCGWEKKNVDPIDTCAKDGTTTVAASNDTVKSGCDGDTGMCYDQT 75

QY 191 PMAVNDNLAYGFAPAAAIISGGESRWCCSCFELFTSTSVAGKKVAVVNTGDLGSSGTG 250

DB 76 PMQVSDSLSYGFAPAAACC-GGESGACCGCYELFTTSGPVNGKKMIVQITNTGDLGSSN-- 132

QY 251 AHFLQMPGGGVIIFNGCCSQMGAPNDGWSRGYGISASDSSLPSALQAGCKKRFNFW 310

DB 133 -QFDLAIPIGGGVIINGCTAOSGAPSDGWSRGYGSRSBSCQLPSGLQAGCQMRDWF 191

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 ANADNPINFTNVKCPSEIIAKTNCNR 218

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 ANADNPINFTNVKCPSEIIAKTNCNR 218

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 ANADNPINFTNVKCPSEIIAKTNCNR 218

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 ANADNPINFTNVKCPSEIIAKTNCNR 218

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 ANADNPINFTNVKCPSEIIAKTNCNR 218

QY 311 KNADNPMTYKEVTCPEKTIATKTCGR 337

DB 192 ANADNPINFTNVKCPSEIIAKTNCNR 218

Matches 131; Conservative 29; Mismatches 42; Indels 5; Gaps 3;

```

QY 132 NGVTRVMDCCKASGMPGKANVSSPVKSCNKGVTAL-SDSNAOAGCNGNSYMCNDNQ 190
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 16 SGTTRVMDCCKSGCMGKADVSKPIDTCADGTRVANSNDTVKSGCDGSGPMICYDQT 75
QY 191 PMAVNDNLAYGFAPAAAIISGGGSRWCCSCFELFTSTSYAGKKMYYQVNTGDLGSSSTG 250
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 76 PMAVNDSYSLGFAPAAAIIS-GGEGAGACCCGYDLFTFTSGPNVNGKKMYYQVNTGDLGSSN-- 132
QY 251 AHFDLQMPGGGVIIFNGCSSQWGPAPNDGWSRYGSISSADCSLPSALQAGCKMRFNMF 310
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 133 -QFDLAIPEGGVGIVNGCTAQSAPSDGWSRYGVSRSRSCQLPSGLQAGCQWRFDWF 191
QY 311 KNADNPSMTYKEVTCPEKITAKTGCGR 337
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 192 QNADNPINPSSVRCPEKITAKTNCNR 218

```

RESULT 12

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QY 09JH85 PRELIMINARY; PRT; 218 AA.
AC 09JH85;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
   protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045178; BAA98048.1; -.
DR HSSP; P43316; 3ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 218 AA; 22680 MW; A600FFB990AD43 CRC64;

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Query Match 41.1%; Score 755; DB 14; Length 218;

Best Local Similarity 65.4%; Pred. No. 6.1e-44;

Matches 136; Conservative 30; Mismatches 36; Indels 6; Gaps 4;

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QY 132 NGVTRVMDCCKASGMPGKANVSSPVKSCNKGVTALSDSNAOAGC-NGNSYMCNDNQ 190
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 16 DGRTRVMDCCKSGCMGKADVSKPIDTCADGTRVANS-AKSACDSGTATMICYDQT 74
QY 191 PMAVNDNLAYGFAPAAAIISGGGSRWCCSCFELFTSTSYAGKKMYYQVNTGDLGSSSTG 250
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 75 PMAVNDSYSLGFAPAAAIIS-GGEGACACCTCYELFTFTSGPNVNGKKMYYQVNTGDLGSSN-- 131
QY 251 AHFDLQMPGGGVIIFNGCSSQWGPAPNDGWSRYGSISSADCSLPSALQAGCKMRFNMF 310
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 132 -QFDLAIPEGGVGIVNGCTAQSAPSDGWSRYGVSRSRSCQLPSGLQAGCQWRFDWF 190
QY 311 KNADNPSMTYKEVTCPEKITAKTGCGR 338
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 191 QNADNPISITFNEVSCPEKITAKTNCNRQ 218

```

RESULT 13

```

QY 09JH94 PRELIMINARY; PRT; 221 AA.
AC 09JH94;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.

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OC Eukaryota.
OX NCBI_TaxID=42452;

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RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
   protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045169; BAA98039.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 221 AA; 23220 MW; 8A84CEB0A8C46372 CRC64;

```

Query Match 41.0%; Score 753.5; DB 14; Length 221;

Best Local Similarity 63.3%; Pred. No. 7.9e-44;

Matches 131; Conservative 30; Mismatches 41; Indels 5; Gaps 3;

```

QY 132 NGVTRVMDCCKASGMPGKANVSSPVKSCNKGVTAL-SDSNAOAGCNGNSYMCNDNQ 190
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 17 SGTTRVMDCCKSGCMGKADVSKPIDTCADGTRVANSNDTVKSGCDGSGPMICYDQT 76
QY 191 PMAVNDNLAYGFAPAAAIISGGGSRWCCSCFELFTSTSYAGKKMYYQVNTGDLGSSSTG 250
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 77 PMAVNDSYSLGFAPAAAIIS-GGEGACACCCGYELFTFTSGPNVNGKKMYYQVNTGDLGSSN-- 133
QY 251 AHFDLQMPGGGVIIFNGCSSQWGPAPNDGWSRYGSISSADCSLPSALQAGCKMRFNMF 310
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 134 -QFDLAIPEGGVGIVNGCTAQSAPSDGWSRYGVSRSRSCQLPSGLQAGCQWRFDWF 192
QY 311 KNADNPSMTYKEVTCPEKITAKTGCGR 337
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 193 QNADNPISITFNEVSCPEKITAKTNCNR 219

```

RESULT 14

```

QY 09JH96 PRELIMINARY; PRT; 220 AA.
AC 09JH96;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
   protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045165; BAA98035.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 220 AA; 23148 MW; 4F0652F8EBD269D5 CRC64;

```

Query Match 40.5%; Score 743.5; DB 14; Length 220;

Best Local Similarity 64.7%; Pred. No. 3.7e-43;

Matches 134; Conservative 24; Mismatches 44; Indels 5; Gaps 3;

```

QY 132 NGVTRVMDCCKASGMPGKANVSSPVKSCNKGVTAL-SDSNAOAGCNGNSYMCNDNQ 190
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 17 SGTTRVMDCCKSGCMGKADVSKPIDTCADGTRVANSNDTVKSGCDGSGPMICYDQT 76
QY 191 PMAVNDNLAYGFAPAAAIISGGGSRWCCSCFELFTSTSYAGKKMYYQVNTGDLGSSSTG 250
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 77 PMAVNDSYSLGFAPAAAIIS-GGEGACACCCGYELFTFTSGPNVNGKKMYYQVNTGDLGSSN-- 133
QY 251 AHFDLQMPGGGVIIFNGCSSQWGPAPNDGWSRYGSISSADCSLPSALQAGCKMRFNMF 310

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Db 134 -QFDLAPGGGVTGYNCTAGSGADWGSRTGVSSRSECQLPSGLQAGCQMRDWF 192
QY 311 KNADNPSTYKEVTCPEKITAKTGCGR 337
Db 193 QNADNPSTINFNVSCEPGLIANTNCRR 219

RESULT 15

Q9P868 PRELIMINARY; PRT; 410 AA.
AC Q9P868;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Endoglucanase 45A.
GN CEL45A.
OS Piriomyces equi.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Piriomyces.
OX NCBI_TaxID=99929;
RN (1)
RP SEQUENCE FROM N. A.
RX MEDLINE=20391845; PubMed=10931904;
RA Eberhardt R. Y., Gilbert H. J., Hazlewood G. P.;
RT "Primary sequence and enzymatic properties of two modular
endoglucanases, Cel45A and Cel45B, from the anaerobic fungus Piriomyces
RT equi.";
RL Microbiology 146:1999-2008(2000).
DR EMBL; AJ277482; CAB92325.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR002883; CBD 5.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02013; CBM_10; 3.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 410 AA; 44380 MW; D813BD9CFD8238DC CRC64;

Query Match 39.6%; Score 727.5; DB 3; Length 410;

Best Local Similarity 38.2%; Pred. No. 8.5e-42;
Matches 160; Conservative 52; Mismatches 90; Indels 117; Gaps 15;

QY 12 LALALGTEMASAECSKLYGQCGGNMNGPTCCESGSTCKVSN----- 54
Db 1 MRLALTSCTIALAASIAKVASACMAQS--QGYNCNNPSTYKEVTCPEKITAKTGCGR 337
QY 55 DY-YSQ-----CLPSGS-----SGN-----KSESAAKK 77
Db 60 DYSYGQNGNESCTGNGSYPCNCNTQATYTDGDMWAFENGWCGIKNSCKQOPONNNQC 119
QY 78 TTTAAHKTTT-----AAHKTTTAAKTTTAAKSTPS 112
Db 120 TGNAGYRCNCNTQATYTTNEGKMAFENGWCGIKNSCKQVTTTTRRTTTTQQOQPT 179
QY 113 NSSSSS-----SGKYSAVSGASGNGVTRYWDCCKKASGWPCKA---NVSSPYKS 160
Db 180 GSGGNSNYPLNPDPFSQ-----TGKTRYWDCCLASCSWQENCKNDGAGVYRS 229
QY 161 CNKGQVTLSD--SN--AOSGNGNSYMCNDNOPWAVNDLAVGFAPAAATSGGESRWC 216
Db 230 CNVDITPTDLSNLMRYKSGNGSVYMCNDQCPMAINDVAVGFVAS-----HEKC 282
QY 217 CSCPFLTFTSTSVAGKKNVQVNTGDLGSGTGAHFDLQMPGGGVGIFNGCSSQWGA 276
Db 283 CTCQRLKFTSGPIAKQKMIQVTTNTGDLSSN--HFDIQMPGGGVGIFDGTSGFGGSY 339
QY 277 DGMGSRYGISISSADCSLPSALQAGCKRNFNFNADNPSTYKEVTCPEKITAKTGC 335
Db 340 Q-WGRYRGISISSAQCANLPOLKAGCEWRFNFKADNPVAVFERVOCPEKITAKTGC 397